

RAW SEQUENCE LISTING

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Application Serial Number: 10/590,426
Source: TFWP
Date Processed by STIC: 09/01/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 09/01/2006

PATENT APPLICATION: US/10/590,426

TIME: 11:55:24

Input Set : A:\P03373US0 sequence listing.txt

Output Set: N:\CRF4\09012006\J590426.raw

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3 <110> APPLICANT: ISIS INNOVATION LIMITED
5 <120> TITLE OF INVENTION: HYDROGEN PEROXIDE OXIDATION
7 <130> FILE REFERENCE: N.91079A SA
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/590,426
C--> 9 <141> CURRENT FILING DATE: 2006-08-23
9 <160> NUMBER OF SEQ ID NOS: 36
11 <170> SOFTWARE: PatentIn version 3.2
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1248
15 <212> TYPE: DNA
16 <213> ORGANISM: Pseudomonas putida
19 <220> FEATURE:
20 <221> NAME/KEY: CDS
21 <222> LOCATION: (1)..(1248)
23 <220> FEATURE:
24 <221> NAME/KEY: misc_feature
25 <222> LOCATION: (4)..(4)
27 <400> SEQUENCE: 1
28 atg acg act gaa acc ata caa agc aac gcc aat ctt gcc cct ctg cca      48
29 Met Thr Thr Glu Thr Ile Gln Ser Asn Ala Asn Leu Ala Pro Leu Pro
30 1          5          10          15
32 ccc cat gtg cca gag cac ctg gta ttc gac ttc gac atg tac aat ccg      96
33 Pro His Val Pro Glu His Leu Val Phe Asp Phe Asp Met Tyr Asn Pro
34          20          25          30
36 tcg aat ctg tct gcc ggc gtg cag gag gcc tgg gca gtt ctg caa gaa      144
37 Ser Asn Leu Ser Ala Gly Val Gln Glu Ala Trp Ala Val Leu Gln Glu
38          35          40          45
40 tca aac gta ccg gat ctg gtg tgg act cgc tgc aac ggc gga cac tgg      192
41 Ser Asn Val Pro Asp Leu Val Trp Thr Arg Cys Asn Gly Gly His Trp
42          50          55          60
44 atc gcc act cgc ggc caa ctg atc cgt gag gcc tat gaa gat tac cgc      240
45 Ile Ala Thr Arg Gly Gln Leu Ile Arg Glu Ala Tyr Glu Asp Tyr Arg
46 65          70          75          80
48 cac ttt tcc agc gag tgc ccg ttc atc cct cgt gaa gcc ggc gaa gcc      288
49 His Phe Ser Ser Glu Cys Pro Phe Ile Pro Arg Glu Ala Gly Glu Ala
50          85          90          95
52 tac gac ttc att ccc acc tcg atg gat ccg ccc gag cag cgc cag ttt      336
53 Tyr Asp Phe Ile Pro Thr Ser Met Asp Pro Pro Glu Gln Arg Gln Phe
54          100          105          110
56 cgt gcg ctg gcc aac caa gtg gtt ggc atg ccg gtg gtg gat aag ctg      384
57 Arg Ala Leu Ala Asn Gln Val Val Gly Met Pro Val Val Asp Lys Leu
58          115          120          125
60 gag aac cgg atc cag gag ctg gcc tgc tcg ctg atc gag agc ctg cgc      432

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61	Glu	Asn	Arg	Ile	Gln	Glu	Leu	Ala	Cys	Ser	Leu	Ile	Glu	Ser	Leu	Arg	
62		130					135					140					
64	ccg	caa	gga	cag	tgc	aac	ttc	acc	gag	gac	tac	gcc	gaa	ccc	ttc	ccg	480
65	Pro	Gln	Gly	Gln	Cys	Asn	Phe	Thr	Glu	Asp	Tyr	Ala	Glu	Pro	Phe	Pro	
66	145					150					155					160	
68	ata	cgc	atc	ttc	atg	ctg	ctc	gca	ggt	cta	ccg	gaa	gaa	gat	atc	ccg	528
69	Ile	Arg	Ile	Phe	Met	Leu	Leu	Ala	Gly	Leu	Pro	Glu	Glu	Asp	Ile	Pro	
70					165					170					175		
72	cac	ttg	aaa	tac	cta	acg	gat	cag	atg	acc	cgt	ccg	gat	ggc	agc	atg	576
73	His	Leu	Lys	Tyr	Leu	Thr	Asp	Gln	Met	Thr	Arg	Pro	Asp	Gly	Ser	Met	
74				180					185					190			
76	acc	ttc	gca	gag	gcc	aag	gag	gcg	ctc	tac	gac	tat	ctg	ata	ccg	atc	624
77	Thr	Phe	Ala	Glu	Ala	Lys	Glu	Ala	Leu	Tyr	Asp	Tyr	Leu	Ile	Pro	Ile	
78			195					200					205				
80	atc	gag	caa	cgc	agg	cag	aag	ccg	gga	acc	gac	gct	atc	agc	atc	gtt	672
81	Ile	Glu	Gln	Arg	Arg	Gln	Lys	Pro	Gly	Thr	Asp	Ala	Ile	Ser	Ile	Val	
82		210				215						220					
84	gcc	aac	ggc	cag	gtc	aat	ggg	cga	ccg	atc	acc	agt	gac	gaa	gcc	aag	720
85	Ala	Asn	Gly	Gln	Val	Asn	Gly	Arg	Pro	Ile	Thr	Ser	Asp	Glu	Ala	Lys	
86	225					230					235				240		
88	agg	atg	tgt	ggc	ctg	tta	ctg	gtc	ggc	ggc	ctg	gat	acg	gtg	gtc	aat	768
89	Arg	Met	Cys	Gly	Leu	Leu	Leu	Val	Gly	Gly	Leu	Asp	Thr	Val	Val	Asn	
90					245					250					255		
92	ttc	ctc	agc	ttc	agc	atg	gag	ttc	ctg	gcc	aaa	agc	ccg	gag	cat	cgc	816
93	Phe	Leu	Ser	Phe	Ser	Met	Glu	Phe	Leu	Ala	Lys	Ser	Pro	Glu	His	Arg	
94				260					265					270			
96	cag	gag	ctg	atc	gag	cgt	ccc	gag	cgt	att	cca	gcc	gct	tgc	gag	gaa	864
97	Gln	Glu	Leu	Ile	Glu	Arg	Pro	Glu	Arg	Ile	Pro	Ala	Ala	Cys	Glu	Glu	
98		275						280					285				
100	cta	ctc	cgg	cgc	ttc	tgc	ctg	gtt	gcc	gat	ggc	cgc	atc	ctc	acc	tcc	912
101	Leu	Leu	Arg	Arg	Phe	Ser	Leu	Val	Ala	Asp	Gly	Arg	Ile	Leu	Thr	Ser	
102		290					295					300					
104	gat	tac	gag	ttt	cat	ggc	gtg	caa	ctg	aag	aaa	ggt	gac	cag	atc	ctg	960
105	Asp	Tyr	Glu	Phe	His	Gly	Val	Gln	Leu	Lys	Lys	Gly	Asp	Gln	Ile	Leu	
106	305					310					315					320	
108	cta	ccg	cag	atg	ctg	tct	ggc	ctg	gat	gag	cgc	gaa	aac	gcc	tgc	ccg	1008
109	Leu	Pro	Gln	Met	Leu	Ser	Gly	Leu	Asp	Glu	Arg	Glu	Asn	Ala	Cys	Pro	
110					325					330					335		
112	atg	cac	gtc	gac	ttc	agt	cgc	caa	aag	gtt	tca	cac	acc	acc	ttt	ggc	1056
113	Met	His	Val	Asp	Phe	Ser	Arg	Gln	Lys	Val	Ser	His	Thr	Thr	Phe	Gly	
114				340					345					350			
116	cac	ggc	agc	cat	ctg	tgc	ctt	ggc	cag	cac	ctg	gcc	cgc	cgg	gaa	atc	1104
117	His	Gly	Ser	His	Leu	Cys	Leu	Gly	Gln	His	Leu	Ala	Arg	Arg	Glu	Ile	
118			355					360					365				
120	atc	gtc	acc	ctc	aag	gaa	tgg	ctg	acc	agg	att	cct	gac	ttc	tcc	att	1152
121	Ile	Val	Thr	Leu	Lys	Glu	Trp	Leu	Thr	Arg	Ile	Pro	Asp	Phe	Ser	Ile	
122		370					375					380					
124	gcc	ccg	ggt	gcc	cag	att	cag	cac	aag	agc	ggc	atc	gtc	agc	ggc	gtg	1200
125	Ala	Pro	Gly	Ala	Gln	Ile	Gln	His	Lys	Ser	Gly	Ile	Val	Ser	Gly	Val	

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126 385          390          395          400
128 cag gca ctc cct ctg gtc tgg gat ccg gcg act acc aaa gcg gta taa      1248
129 Gln Ala Leu Pro Leu Val Trp Asp Pro Ala Thr Thr Lys Ala Val
130          405          410          415
133 <210> SEQ ID NO: 2
134 <211> LENGTH: 415
135 <212> TYPE: PRT
136 <213> ORGANISM: Pseudomonas putida
138 <400> SEQUENCE: 2
140 Met Thr Thr Glu Thr Ile Gln Ser Asn Ala Asn Leu Ala Pro Leu Pro
141 1          5          10          15
144 Pro His Val Pro Glu His Leu Val Phe Asp Phe Asp Met Tyr Asn Pro
145          20          25          30
148 Ser Asn Leu Ser Ala Gly Val Gln Glu Ala Trp Ala Val Leu Gln Glu
149          35          40          45
152 Ser Asn Val Pro Asp Leu Val Trp Thr Arg Cys Asn Gly Gly His Trp
153          50          55          60
156 Ile Ala Thr Arg Gly Gln Leu Ile Arg Glu Ala Tyr Glu Asp Tyr Arg
157 65          70          75          80
160 His Phe Ser Ser Glu Cys Pro Phe Ile Pro Arg Glu Ala Gly Glu Ala
161          85          90          95
164 Tyr Asp Phe Ile Pro Thr Ser Met Asp Pro Pro Glu Gln Arg Gln Phe
165          100         105         110
168 Arg Ala Leu Ala Asn Gln Val Val Gly Met Pro Val Val Asp Lys Leu
169          115         120         125
172 Glu Asn Arg Ile Gln Glu Leu Ala Cys Ser Leu Ile Glu Ser Leu Arg
173          130         135         140
176 Pro Gln Gly Gln Cys Asn Phe Thr Glu Asp Tyr Ala Glu Pro Phe Pro
177 145         150         155         160
180 Ile Arg Ile Phe Met Leu Leu Ala Gly Leu Pro Glu Glu Asp Ile Pro
181          165         170         175
184 His Leu Lys Tyr Leu Thr Asp Gln Met Thr Arg Pro Asp Gly Ser Met
185          180         185         190
188 Thr Phe Ala Glu Ala Lys Glu Ala Leu Tyr Asp Tyr Leu Ile Pro Ile
189          195         200         205
192 Ile Glu Gln Arg Arg Gln Lys Pro Gly Thr Asp Ala Ile Ser Ile Val
193          210         215         220
196 Ala Asn Gly Gln Val Asn Gly Arg Pro Ile Thr Ser Asp Glu Ala Lys
197 225         230         235         240
200 Arg Met Cys Gly Leu Leu Leu Val Gly Gly Leu Asp Thr Val Val Asn
201          245         250         255
204 Phe Leu Ser Phe Ser Met Glu Phe Leu Ala Lys Ser Pro Glu His Arg
205          260         265         270
208 Gln Glu Leu Ile Glu Arg Pro Glu Arg Ile Pro Ala Ala Cys Glu Glu
209          275         280         285
212 Leu Leu Arg Arg Phe Ser Leu Val Ala Asp Gly Arg Ile Leu Thr Ser
213          290         295         300
216 Asp Tyr Glu Phe His Gly Val Gln Leu Lys Lys Gly Asp Gln Ile Leu
217 305         310         315         320

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220 Leu Pro Gln Met Leu Ser Gly Leu Asp Glu Arg Glu Asn Ala Cys Pro
221           325           330           335
224 Met His Val Asp Phe Ser Arg Gln Lys Val Ser His Thr Thr Phe Gly
225           340           345           350
228 His Gly Ser His Leu Cys Leu Gly Gln His Leu Ala Arg Arg Glu Ile
229           355           360           365
232 Ile Val Thr Leu Lys Glu Trp Leu Thr Arg Ile Pro Asp Phe Ser Ile
233           370           375           380
236 Ala Pro Gly Ala Gln Ile Gln His Lys Ser Gly Ile Val Ser Gly Val
237 385           390           395           400
240 Gln Ala Leu Pro Leu Val Trp Asp Pro Ala Thr Thr Lys Ala Val
241           405           410           415
244 <210> SEQ ID NO: 3
245 <211> LENGTH: 4957
246 <212> TYPE: DNA
247 <213> ORGANISM: Bacillus megaterium
250 <220> FEATURE:
251 <221> NAME/KEY: CDS
252 <222> LOCATION: (1541)..(4690)
254 <400> SEQUENCE: 3
255 agatctttat gaagacatag ctgcagaaga aaaagcaaga gctacatatc aatggttaat      60
257 tgatatatca gatgatcccg atttaaacga cagcttacga tttttacgag aaagagagat      120
259 tgttcactca cagcggttcc gcgaggccgt ggagatttta aaagatgaca gagacaggaa      180
261 gaaaatcttt taactagtaa aaaaacatcc cccttggcga atgcaaacga aaggagggat      240
263 gttttttggt gtgactgcgt tgattatgct ctagaactgc agtgacaaga aacaaccttt      300
265 aatttccctt caacatcttt ccaaactcgc gtataactgt attcacctcc aatagattca      360
267 ccggttgcca gtgccccatt taacgctact tttgtaacgg taacggcaag ttcttgaaac      420
269 agtttaactt cttgttccaa cacttccatg cccgctatat caagactttt tgaacgatga      480
271 acatttatat cttcttcttt tgacaaccat tgcccaaggt gattcacaaa aataagctca      540
273 tctgaaagta attcttctaa tagctctatg ttattagaaa gcatggctga gcgaagcatt      600
275 tcttcgtatt ctataactct tgcttgattc atttttaatc ctcttttacg ccttgtgtaa      660
277 ctcttttcta tttccacggt gcttttcctt taaacttctt tcattaataa ttcgtgctaa      720
279 attatgttaa tagaggggat aagtggacta attttctgta agcactaaat attctgaaat      780
281 actctgttaa ttacctttaa atggtataaa attagaatga aagaaccttt tctttccact      840
283 tttctagtta tctttttact attaagatgc agttttttat acttgtaatt gtagcggaat      900
285 gaacgttcat tccgtttttg aaaagaggtg ataaagtgga atctactcca acaaaacaaa      960
287 aagcgatttt ttctgcttcg cttctgctgt ttgcagaaag agggtttgat gcaaccacga     1020
289 tgccaatgat tgcagagaat gccaaagtag gagcaggaac aatttatcgc tactttaaaa     1080
291 ataaagaaag ctttgtaaat gaattattcc aacagcacgt aaacgagttt ttacagtgca     1140
293 ttgaaagcgg tctggcaaac gagagagatg gataccgaga tgggtttcat catatctttg     1200
295 aaggatatgt gacatttact aaaaaccatc ctctgtgctt tggatttatt aaaactcata     1260
297 gccaaggaac ttttttaaca gaagagagcc gcttagcata tcaaaagctg gtggaatttg     1320
299 tttgtacgtt cttcagagaa ggacaaaagc aagggtgtgat tagaaatctt cctgaaaatg     1380
301 cgctaattgc tattttattt ggaagtcca tggaagtata tgaaatgatt gaaaatgact     1440
303 acttatcttt aactgatgaa cttcttaccg gtgtagaaga gagtctgtgg gcagcactta     1500
305 gcagacaatc atgaaactta acaagtgaaa gagggataac atg aca att aaa gaa     1555
306                                     Met Thr Ile Lys Glu
307                                     1               5
309 atg cct cag cca aaa acg ttt gga gag ctt aaa aat tta ccg tta tta     1603

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310	Met	Pro	Gln	Pro	Lys	Thr	Phe	Gly	Glu	Leu	Lys	Asn	Leu	Pro	Leu	Leu	
311					10					15					20		
313	aac	aca	gat	aaa	ccg	gtt	caa	gct	ttg	atg	aaa	att	gcg	gat	gaa	tta	1651
314	Asn	Thr	Asp	Lys	Pro	Val	Gln	Ala	Leu	Met	Lys	Ile	Ala	Asp	Glu	Leu	
315				25					30				35				
317	gga	gaa	atc	ttt	aaa	ttc	gag	gcg	cct	ggg	cgt	gta	acg	cg	tac	tta	1699
318	Gly	Glu	Ile	Phe	Lys	Phe	Glu	Ala	Pro	Gly	Arg	Val	Thr	Arg	Tyr	Leu	
319			40					45					50				
321	tca	agt	cag	cgt	cta	att	aaa	gaa	gca	tgc	gat	gaa	tca	cg	ttt	gat	1747
322	Ser	Ser	Gln	Arg	Leu	Ile	Lys	Glu	Ala	Cys	Asp	Glu	Ser	Arg	Phe	Asp	
323		55					60				65						
325	aaa	aac	tta	agt	caa	gcg	ctt	aaa	ttt	gta	cgt	gat	ttt	gca	gga	gac	1795
326	Lys	Asn	Leu	Ser	Gln	Ala	Leu	Lys	Phe	Val	Arg	Asp	Phe	Ala	Gly	Asp	
327	70					75				80					85		
329	ggg	tta	ttt	aca	agc	tgg	acg	cat	gaa	aaa	aat	tgg	aaa	aaa	gcg	cat	1843
330	Gly	Leu	Phe	Thr	Ser	Trp	Thr	His	Glu	Lys	Asn	Trp	Lys	Lys	Ala	His	
331					90					95					100		
333	aat	atc	tta	ctt	cca	agc	ttc	agt	cag	cag	gca	atg	aaa	ggc	tat	cat	1891
334	Asn	Ile	Leu	Leu	Pro	Ser	Phe	Ser	Gln	Gln	Ala	Met	Lys	Gly	Tyr	His	
335				105					110				115				
337	gcg	atg	atg	gtc	gat	atc	gcc	gtg	cag	ctt	gtt	caa	aag	tgg	gag	cgt	1939
338	Ala	Met	Met	Val	Asp	Ile	Ala	Val	Gln	Leu	Val	Gln	Lys	Trp	Glu	Arg	
339			120					125				130					
341	cta	aat	gca	gat	gag	cat	att	gaa	gta	ccg	gaa	gac	atg	aca	cgt	tta	1987
342	Leu	Asn	Ala	Asp	Glu	His	Ile	Glu	Val	Pro	Glu	Asp	Met	Thr	Arg	Leu	
343		135					140					145					
345	acg	ctt	gat	aca	att	ggg	ctt	tgc	ggc	ttt	aac	tat	cg	ttt	aac	agc	2035
346	Thr	Leu	Asp	Thr	Ile	Gly	Leu	Cys	Gly	Phe	Asn	Tyr	Arg	Phe	Asn	Ser	
347	150					155				160					165		
349	ttt	tac	cga	gat	cag	cct	cat	cca	ttt	att	aca	agt	atg	gtc	cgt	gca	2083
350	Phe	Tyr	Arg	Asp	Gln	Pro	His	Pro	Phe	Ile	Thr	Ser	Met	Val	Arg	Ala	
351				170					175				180				
353	ctg	gat	gaa	gca	atg	aac	aag	ctg	cag	cga	gca	aat	cca	gac	gac	cca	2131
354	Leu	Asp	Glu	Ala	Met	Asn	Lys	Leu	Gln	Arg	Ala	Asn	Pro	Asp	Asp	Pro	
355			185					190				195					
357	gct	tat	gat	gaa	aac	aag	cg	cag	ttt	caa	gaa	gat	atc	aag	gtg	atg	2179
358	Ala	Tyr	Asp	Glu	Asn	Lys	Arg	Gln	Phe	Gln	Glu	Asp	Ile	Lys	Val	Met	
359			200				205					210					
361	aac	gac	cta	gta	gat	aaa	att	att	gca	gat	cg	aaa	gca	agc	ggg	gaa	2227
362	Asn	Asp	Leu	Val	Asp	Lys	Ile	Ile	Ala	Asp	Arg	Lys	Ala	Ser	Gly	Glu	
363		215					220					225					
365	caa	agc	gat	gat	tta	tta	acg	cat	atg	cta	aac	gga	aaa	gat	cca	gaa	2275
366	Gln	Ser	Asp	Asp	Leu	Leu	Thr	His	Met	Leu	Asn	Gly	Lys	Asp	Pro	Glu	
367	230					235				240					245		
369	acg	ggg	gag	ccg	ctt	gat	gac	gag	aac	att	cg	tat	caa	att	att	aca	2323
370	Thr	Gly	Glu	Pro	Leu	Asp	Asp	Glu	Asn	Ile	Arg	Tyr	Gln	Ile	Ile	Thr	
371				250				255				260					
373	ttc	tta	att	gcg	gga	cac	gaa	aca	aca	agt	ggg	ctt	tta	tca	ttt	gcg	2371
374	Phe	Leu	Ile	Ala	Gly	His	Glu	Thr	Thr	Ser	Gly	Leu	Leu	Ser	Phe	Ala	

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date